

SEQUENCE LISTING

<110> CHANG, Y-H
VETRO, J.A.
MICKA, W.S.

<120> Dominant Negative Variants of Methionine Aminopeptidase
2 ("MetAP2") and Clinical Uses Therefor

<130> 16153-8007

<140>
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<160> 26

<170> PatentIn Ver. 2.0

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Lys Lys Lys Lys Lys Lys
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 35 40 45
 Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
 50 55 60
 Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
 65 70 75 80
 Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Gln Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala
35 40 45

Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Leu
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 35 40 45
 Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50 55 60
 Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65 70 75 80
 Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95
 Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110
 Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125
 Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
 130 135 140
 Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
 145 150 155 160
 Gly Xaa Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala Xaa Phe Thr
 165 170 175
 Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
 180 185 190
 Val Xaa Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Xaa Ser Ala Phe
 195 200 205
 Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220
 Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
 225 230 235 240
 Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255
 Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Xaa Cys
 260 265 270
 Gly Xaa Ser Ile Ala Pro Tyr Arg Xaa Xaa Gly Gly Lys Ser Val Pro
 275 280 285
 Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300
 Ala Ile Xaa Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
 305 310 315 320

Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
 325 330 335

Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
 340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
 355 360 365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380

Gln Asp Xaa Pro Pro Xaa Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
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tgtgacctgt atcctaattgg tggatccc aaaggacaag aatgcgaata cccacccaca 420
caagatgggc gaacagctgc ttggagaact acaagtgaag aaaagaaagc attagatcag 480
gcaagtgaag agatttgaa tgatttcgaa gaagctgcag aagcacatcg acaagtttaga 540
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gaagactgtt cacgcaagtt aataaaagag aatggattaa atgcaggcct ggcatttcct 660
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gatcgcttgg gagaaaagttt atacttgatg gctctgaaga atctgtgtga cttgggcatt 1320
gtagatccat atccaccatt atgtgacatt aaaggatcat atacagcgca atttgaacat 1380
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 50 55 60
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 65 70 75 80
 Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Gln Tyr
 325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
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 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
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 35 40 45
 Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
 50 55 60
 Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80
 Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
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 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
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 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
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 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
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Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
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 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
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 Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
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 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
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 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
 325 330 335
 Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
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 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
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 35 40 45

Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50 55 60

Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65 70 75 80

Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95

Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125

Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
 130 135 140

Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
 145 150 155 160

Gly Phe Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala His Phe Thr
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Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
 180 185 190

Val Asp Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Asp Ser Ala Phe
 195 200 205

Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220

Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
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Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255

Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Leu Cys
 260 265 270

Gly His Ser Ile Ala Pro Tyr Arg Ile His Gly Gly Lys Ser Val Pro
 275 280 285

Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300

Ala Ile Glu Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
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Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
 325 330 335

Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
 340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
 355 360 365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380

Gln Asp Tyr Pro Pro Leu Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
 385 390 395 400

Phe Glu His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
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Lys Gly Asp Asp Tyr Gly Lys Met Arg Phe Gln Met Ala Ser Ser Leu
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Gly Ile Ile Leu Leu
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Lys Lys Lys Lys Lys Lys
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Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu.
 20 25 30

Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
 35 40 45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
 50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
 85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
 100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Cys
 450 455 460
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 465 470 475 480

<210> 17
 <211> 480

<212> PRT

<213> Rat MetAP2

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 1 5 10 15

Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
 20 25 30

Glu Ala Ala Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala
 35 40 45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
 50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
 85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
 100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270

Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
 325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Cys
 450 455 460

Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 18

<211> 1944

<212> DNA

<213> Rat MetAP2 variant

<220>

<221> misc_feature

<222> (779)

<223> Any nucleotide

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 gccacctgaa tcgcgacctg gatccagacg acagggaaga gggAACCTCC agcacggcc 180
 aggaagccgc caagaagaaa agacccaaga agaagaaggg caaaggggct gtgtcagcag 240
 ggcacaacaaga acttgataaa gaatccggaa cctcagtgga cgaagtagca aaacagttgg 300
 agagacaaga actggaggag aaagagaaaat atgatgacga tgaagatgga gatgggtatg 360
 gtatgggtgc agctggaaag aagaagaaaa agaagaagaa gaagagagga ccaagagttc 420
 aaacagaccc tccctcagtt ccaatatgtg acctgtatcc taatgggtta tttcccaaag 480
 gacaagagtg tgaataccca cccaccccaag atggggccgac agctgttgg agaaccacaaa 540
 gtgaagagaa aaaggcgcta gaccaggctgatggaggat ttggAACGAC ttccgagaag 600
 ctggcaagc acacccggaa gtttagaaat acgtcatgatggatcaag cttggatgatg 660
 caatgataga aatatgttag aagtggaaactgttcccg aaagctcata aaggagaatg 720
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 aatatgacat attattaaaaa gctgtaaaag atgccaccaa tactggaata aagtgtgcgg 960
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tgaagaacct gtgtgacttg ggcattgttag atccatatcc accactctgt gacattaaag 1440
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 cagcagagga gatgactatt aaaacttagt ccaaagccaa ctcaacgtct ttattttcta 1560
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 taatttaacca aggaaaaggc tttcaagact ttactgttaa ctgtttctcc cgtctaggaa 1740
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<210> 19

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
transit peptide

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<210> 20

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide

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40

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 21

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35

<210> 22

<211> 11

<212> PRT

<213> Artificial Sequence

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peptide

<400> 22

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1 5 10

<210> 23

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic peptide

<400> 23

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<210> 24

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic peptide

<400> 24

Met Gly Met Met
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<210> 25

<211> 63

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 25

cacactcgac cgcgatgtac tactactact actactacta ctactacggg ccagatatac 60
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<210> 26

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 26

cacagaattc cccgcatccc cagcatgcct gctattg

37